



IFWO

RAW SEQUENCE LISTING

DATE: 08/31/2004

PATENT APPLICATION: US/10/795,933

TIME: 12:53:28

Input Set : N:\Crfr3\RULE60\10795933.raw
 Output Set: N:\CRF4\08312004\J795933.raw

1 <110> APPLICANT: Zavada, Jan
 2 Pastorekova, Silvia
 3 Pastorek, Jaromir
 4 <120> TITLE OF INVENTION: MN Gene and Protein
 5 <130> FILE REFERENCE: D-0021-2
 6 <140> CURRENT APPLICATION NUMBER: US/10/795,933
 7 <141> CURRENT FILING DATE: 2004-03-08
 8 <150> PRIOR APPLICATION NUMBER: US/08/260,190
 9 <151> PRIOR FILING DATE: 1994-06-15
 10 <150> PRIOR APPLICATION NUMBER: 08/177,093
 11 <151> PRIOR FILING DATE: 1993-12-30
 12 <150> PRIOR APPLICATION NUMBER: 07/964,589
 13 <151> PRIOR FILING DATE: 1992-10-21
 14 <150> PRIOR APPLICATION NUMBER: PV-709-92
 15 <151> PRIOR FILING DATE: 1992-03-11
 16 <160> NUMBER OF SEQ ID NOS: 26
 17 <170> SOFTWARE: PatentIn Ver. 2.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1399
 21 <212> TYPE: DNA
 22 <213> ORGANISM: HUMAN
 23 <220> FEATURE:
 24 <221> NAME/KEY: CDS
 25 <222> LOCATION: (1)..(1266)
 26 <400> SEQUENCE: 1
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 Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro Leu Gly Gly Ser
 1 5 10 15
 tct ggg gaa gat gac cca ctg ggc gag gag gat ctg ccc agt gaa gag 96
 Ser Gly Glu Asp Asp Pro Leu Gly Glu Asp Leu Pro Ser Glu Glu
 20 25 30
 gat tca ccc aga gag gag gat cca ccc gga gag gag gat cta cct gga 144
 Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu Glu Asp Leu Pro Gly
 35 40 45
 gag gag gat cta cct gga gag gag gat cta cct gaa gtt aag cct aaa 192
 Glu Glu Asp Leu Pro Gly Glu Asp Leu Pro Glu Val Lys Pro Lys
 50 55 60
 tca gaa gaa gag ggc tcc ctg aag tta gag gat cta cct act gtt gag 240
 Ser Glu Glu Gly Ser Leu Lys Leu Glu Asp Leu Pro Thr Val Glu
 65 70 75 80
 gct cct gga gat cct caa gaa ccc cag aat aat gcc cac agg gac aaa 288
 Ala Pro Gly Asp Pro Glu Pro Gln Asn Asn Ala His Arg Asp Lys
 85 90 95

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45	gaa ggg gat gac cag agt cat tgg cgc tat gga ggc gac ccg ccc tgg	336
46	Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp	
47	100 105 110	
48	ccc cggtc cca gcc tgc gcg ggc cgc ttc cag tcc ccg gtg gat	384
49	Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp	
50	115 120 125	
51	atc cgc ccc cag ctc gcc gcc ttc tgc ccc ctg cgc ccc ctg gaa	432
52	Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu	
53	130 135 140	
54	ctc ctg ggc ttc cag ctc ccg cca gaa ctg cgc ctg cgc aac	480
55	Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn	
56	145 150 155 160	
57	aat ggc cac agt gtg caa ctg acc ctg cct cct ggg cta gag atg gct	528
58	Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala	
59	165 170 175	
60	ctg ggt ccc ggg cggt tac cgg gct ctg cag ctg cat ctg cac tgg	576
61	Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp	
62	180 185 190	
63	ggg gct gca ggt cgt ccg ggc tcg gag cac act gtg gaa ggc cac cgt	624
64	Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg	
65	195 200 205	
66	tcc cct gcc gag atc cac gtg gtt cac ctc agc acc gcc ttt gcc aga	672
67	Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ala Arg	
68	210 215 220	
69	gtt gac gag gcc ttg ggg cgc ccg gga ggc ctg gcc gtg ttg gcc gcc	720
70	Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala	
71	225 230 235 240	
72	ttt ctg gag gag ggc ccg gaa gaa aac agt gcc tat gag cag ttg ctg	768
73	Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Gln Leu Leu	
74	245 250 255	
75	tct cgc ttg gaa gaa atc gct gag gaa ggc tca gag act cag gtc cca	816
76	Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu Thr Gln Val Pro	
77	260 265 270	
78	gga ctg gac ata tct gca ctc ctg ccc tct gac ttc agc cgc tac ttc	864
79	Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe Ser Arg Tyr Phe	
80	275 280 285	
81	caa tat gag ggg tct ctg act aca ccg ccc tgt gcc cag ggt gtc atc	912
82	Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala Gln Gly Val Ile	
83	290 295 300	
84	tgg act gtg ttt aac cag aca gtg atg ctg agt gct aag cag ctc cac	960
85	Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala Lys Gln Leu His	
86	305 310 315 320	
87	acc ctc tct gac acc ctg tgg gga cct ggt gac tct cgg cta cag ctg	1008
88	Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu	
89	325 330 335	
90	aac ttc cga gcg acg cag cct ttg aat ggg cga gtg att gag gcc tcc	1056
91	Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser	
92	340 345 350	
93	ttc cct gct gga gtg gac agc agt cct cgg gct gct gag cca gtc cag	1104

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94 Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala Glu Pro Val Gln
95 355 360 365
96 ctg aat tcc tgc ctg gct ggt gac atc cta gcc ctg gtt ttt ggc 1152
97 Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu Ala Leu Val Phe Gly
98 370 375 380
99 ctc ctt ttt gct gtc acc agc gtc gcg ttc ctt gtg cag atg aga agg 1200
100 Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg
101 385 390 395 400
102 cag cac aga agg gga acc aaa ggg ggt gtg agc tac cgc cca gca gag 1248
103 Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu
104 405 410 415
105 gta gcc gag act gga gcc tagaggctgg atcttggaga atgtgagaag 1296
106 Val Ala Glu Thr Gly Ala
107 420
108 ccagccagag gcatctgagg gggagccggt aactgtcctg tcctgctcat tatgccactt 1356
109 ccttttaact gccaagaaat ttttaaaat aaatatttat aat 1399
111 <210> SEQ ID NO: 2
112 <211> LENGTH: 422
113 <212> TYPE: PRT
114 <213> ORGANISM: HUMAN
115 <400> SEQUENCE: 2
116 Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro Leu Gly Gly Ser
117 1 5 10 15
118 Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp Leu Pro Ser Glu Glu
119 20 25 30
120 Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu Glu Asp Leu Pro Gly
121 35 40 45
122 Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Glu Val Lys Pro Lys
123 50 55 60
124 Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp Leu Pro Thr Val Glu
125 65 70 75 80
126 Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn Ala His Arg Asp Lys
127 85 90 95
128 Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp
129 100 105 110
130 Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp
131 115 120 125
132 Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu
133 130 135 140
134 Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn
135 145 150 155 160
136 Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala
137 165 170 175
138 Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp
139 180 185 190
140 Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg
141 195 200 205
142 Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ala Arg
143 210 215 220

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144 Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala
 145 225 230 235 240
 146 Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Gln Leu Leu
 147 245 250 255
 148 Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu Thr Gln Val Pro
 149 260 265 270
 150 Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe Ser Arg Tyr Phe
 151 275 280 285
 152 Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala Gln Gly Val Ile
 153 290 295 300
 154 Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala Lys Gln Leu His
 155 305 310 315 320
 156 Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu
 157 325 330 335
 158 Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser
 159 340 345 350
 160 Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala Glu Pro Val Gln
 161 355 360 365
 162 Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu Ala Leu Val Phe Gly
 163 370 375 380
 164 Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg
 165 385 390 395 400
 166 Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu
 167 405 410 415
 168 Val Ala Glu Thr Gly Ala
 169 420
 171 <210> SEQ ID NO: 3
 172 <211> LENGTH: 29
 173 <212> TYPE: DNA
 174 <213> ORGANISM: HUMAN
 175 <400> SEQUENCE: 3
 176 cgccccagtgg gtcatcttcc ccagaagag 29
 178 <210> SEQ ID NO: 4
 179 <211> LENGTH: 19
 180 <212> TYPE: DNA
 181 <213> ORGANISM: HUMAN
 182 <400> SEQUENCE: 4
 183 ggaatcctcc tgcattccgg 19
 185 <210> SEQ ID NO: 5
 186 <211> LENGTH: 1522
 187 <212> TYPE: DNA
 188 <213> ORGANISM: HUMAN
 189 <220> FEATURE:
 190 <221> NAME/KEY: CDS
 191 <222> LOCATION: (13)..(1389)
 192 <220> FEATURE:
 193 <221> NAME/KEY: mat_peptide
 194 <222> LOCATION: (124)..(1389)
 195 <400> SEQUENCE: 5

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Input Set : N:\Crf3\RULE60\10795933.raw
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196	acagtca	gcc	gc	atg	gct	ccc	ctg	tgc	ccc	agc	ccc	tgg	ctc	cct	ctg	ttg	51
197																	
198																	
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/31/2004
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 36,37,41,42,46,47

Seq#:19; N Pos. 7

Seq#:23; N Pos. 1974,2346

Seq#:25; Xaa Pos. 3,4

Seq#:26; Xaa Pos. 3,4

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10795933.raw
Output Set: N:\CRF4\08312004\J795933.raw

L:373 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:9
L:373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:457 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:19
L:457 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:527 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:23
L:527 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:1920
M:341 Repeated in SeqNo=23
L:597 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:25
L:597 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
L:608 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:26
L:608 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0